



10992\_29 ST25.txt  
SEQUENCE LISTING

<110> Institut de Recherches Cliniques de Montreal  
Seidah, Nabil  
Chrétien, Michel  
Marcinkiewicz, Mieczyslaw  
Laaksonen, Reijo  
Davignon, Jean

<120> MAMMALIAN SUBTILISIN/KEXIN ISOZYME SKI-1: A PROPROTEIN CONVERTASE  
WITH A UNIQUE CLEAVAGE SPECIFICITY

<130> 10992.29

<140> US 09/830,837  
<141> 1999-11-04

<150> PCT/CA1999/01058  
<151> 1999-11-04

<150> CA 2,249,648  
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His Ile Phe Arg Val Phe Thr Asn Asn Gln Val Ser Tyr Thr Ser Trp  
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Phe Leu Asp Ala Phe Asn Tyr Ala Ile Leu Lys Lys Met Asp Val Leu  
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Asn Leu Ser Ile Gly Gly Pro Asp Phe Met Asp His Pro Phe Val Asp  
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 Tyr Leu Ala Ile Ser Ile Ser Val Thr Lys Lys Ala Ala Ser Trp Glu  
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 Thr Glu Leu Lys Asn Gly Ala Glu His Thr Ser Thr Val Lys Leu Pro  
 595 600 605  
 Ile Lys Val Lys Ile Ile Pro Thr Pro Pro Arg Ser Lys Arg Val Leu  
 610 615 620  
 Trp Asp Gln Tyr His Asn Leu Arg Tyr Pro Pro Gly Tyr Phe Pro Arg  
 625 630 635 640  
 Asp Asn Leu Arg Met Lys Asn Asp Pro Leu Asp Trp Asn Gly Asp His  
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Val His Thr Asn Phe Arg Asp Met Tyr Gln His Leu Arg Ser Met Gly  
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Thr	Pro	Gln	Arg	Lys	Val	Phe	Arg	Ser	Leu	Lys	Phe	Ala	Glu	Ser	Asn		
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Pro	Ile	Val	Pro	Cys	Asn	Glu	Thr	Arg	Trp	Ser	Gln	Lys	Trp	Gln	Ser		
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gca gag aca gag tta cac agt ggt gcg gag cac act tcc acc gtg aag Ala Glu Thr Glu Leu His Ser Gly Ala Glu His Thr Ser Thr Val Lys 595 600 605	1825
ctg ccc atc aag gtg aag atc att ccc acc cct cct cgg agc aag aga Leu Pro Ile Lys Val Lys Ile Ile Pro Thr Pro Pro Arg Ser Lys Arg 610 615 620	1873
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gcc aca cag tat ggc act ttg ctg ctg gtg gac agt gag gaa gag tac Ala Thr Gln Tyr Gly Thr Leu Leu Leu Val Asp Ser Glu Glu Glu Tyr 690 695 700	2113
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aaa gta gtg tta ccc aac ttt cga tcc aat cgc cct caa gtg aga cct Lys Val Val Leu Pro Asn Phe Arg Ser Asn Arg Pro Gln Val Arg Pro 960 965 970	2929
ttg tcc cct gga gag agt ggt gcc tgg gac att cct gga ggg atc atg Leu Ser Pro Gly Glu Ser Gly Ala Trp Asp Ile Pro Gly Gly Ile Met 975 980 985 990	2977
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Ser Thr Val Val Glu Tyr Glu Tyr Ile Val Ala Phe Asn Gly Tyr Phe  
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Thr Ala Lys Ala Arg Asn Ser Phe Ile Ser Ser Ala Leu Lys Ser Ser  
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Glu Val Glu Asn Trp Arg Ile Ile Pro Arg Asn Asn Pro Ser Ser Asp  
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Tyr Pro Ser Asp Phe Glu Val Ile Gln Ile Lys Glu Lys Gln Lys Ala  
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Gly Leu Leu Thr Leu Glu Asp His Pro Asn Ile Lys Arg Val Thr Pro  
Page 15

115

120

125

Gln Arg Lys Val Phe Arg Ser Leu Lys Phe Ala Glu Ser Asn Pro Ile  
 130 135 140

Val Pro Cys Asn Glu Thr Arg Trp Ser Gln Lys Trp Gln Ser Ser Arg  
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Thr Gly Arg His Ser Ser Arg Arg Leu Leu Arg Ala Ile Pro Arg Gln  
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Gly Ala Asn Val Arg Val Ala Val Phe Asp Thr Gly Leu Ser Glu Lys  
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His Pro His Phe Lys Asn Val Lys Glu Arg Thr Asn Trp Thr Asn Glu  
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Arg Thr Leu Asp Asp Gly Leu Gly His Gly Thr Phe Val Ala Gly Val  
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His Ile Phe Arg Val Phe Thr Asn Asn Gln Val Ser Tyr Thr Ser Trp  
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Phe Leu Asp Ala Phe Asn Tyr Ala Ile Leu Lys Lys Met Asp Val Leu  
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Asn Leu Ser Ile Gly Gly Pro Asp Phe Met Asp His Pro Phe Val Asp  
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Lys Val Trp Glu Leu Thr Ala Asn Asn Val Ile Met Val Ser Ala Ile  
 325 330 335

Gly Asn Asp Gly Pro Leu Tyr Gly Thr Leu Asn Asn Pro Ala Asp Gln  
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Met Asp Val Ile Gly Val Gly Gly Ile Asp Phe Glu Asp Asn Ile Ala  
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 Ser Pro Val Val Ala Gly Ala Val Thr Leu Leu Val Ser Thr Val Gln  
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 Lys Arg Glu Leu Val Asn Pro Ala Ser Val Lys Gln Ala Leu Ile Ala  
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 Met Trp Pro Tyr Cys Ser Gln Pro Ile Tyr Tyr Gly Gly Met Pro Thr  
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 Val Asp Lys Pro Glu Trp Arg Pro Tyr Leu Pro Gln Asn Gly Asp Asn  
 530 535 540  
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 545 550 555 560  
 Tyr Leu Ala Ile Ser Ile Ser Val Thr Lys Lys Ala Ala Ser Trp Glu  
 565 570 575  
 Gly Ile Ala Gln Gly His Ile Met Ile Thr Val Ala Ser Pro Ala Glu  
 580 585 590  
 Thr Glu Leu His Ser Gly Ala Glu His Thr Ser Thr Val Lys Leu Pro  
 595 600 605  
 Ile Lys Val Lys Ile Ile Pro Thr Pro Pro Arg Ser Lys Arg Val Leu  
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Trp Asp Gln Tyr His Asn Leu Arg Tyr Pro Pro Gly Tyr Phe Pro Arg  
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Asp Asn Leu Arg Met Lys Asn Asp Pro Leu Asp Trp Asn Gly Asp His  
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Val His Thr Asn Phe Arg Asp Met Tyr Gln His Leu Arg Ser Met Gly  
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Tyr Phe Val Glu Val Leu Gly Ala Pro Phe Thr Cys Phe Asp Ala Thr  
675 680 685

Gln Tyr Gly Thr Leu Leu Leu Val Asp Ser Glu Glu Glu Tyr Phe Pro  
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Glu Glu Ile Ala Lys Leu Arg Arg Asp Val Asp Asn Gly Leu Ser Leu  
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Val Ile Phe Ser Asp Trp Tyr Asn Thr Ser Val Met Arg Lys Val Lys  
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Phe Tyr Asp Glu Asn Thr Arg Gln Trp Trp Met Pro Asp Thr Gly Gly  
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Met Tyr Tyr Ala Ser Gly Cys Ser Ile Ala Lys Phe Pro Glu Asp Gly  
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Gln Glu Thr Ala Val Val Glu Asn Val Pro Ile Leu Gly Leu Tyr Gln  
820 825 830

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835 840 845

Cys Leu Asp Asp Ser His Arg Gln Lys Asp Cys Phe Trp Leu Leu Asp  
850 855 860

Ala Leu Leu Gln Tyr Thr Ser Tyr Gly Val Thr Pro Pro Ser Leu Ser  
Page 18

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Val Leu Leu Cys Gly Lys Lys His Leu Gly Asp Arg Leu Glu Lys Lys
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Ser Phe Glu Lys Ala Pro Cys Pro Gly Cys Ser His Leu Thr Leu Lys
                30          35          40

gtg gaa ttc tca tca aca gtt gtg gaa tat gaa tat att gtg gct ttc 676
Val Glu Phe Ser Ser Thr Val Val Glu Tyr Glu Tyr Ile Val Ala Phe
                45          50          55          60

aat gga tac ttt aca gcc aaa gct aga aat tca ttt att tca agt gcc 724
Asn Gly Tyr Phe Thr Ala Lys Ala Arg Asn Ser Phe Ile Ser Ser Ala
                65          70          75

ctg aag agc agt gaa gta gac aat tgg aga att ata cct cga aac aat 772
Leu Lys Ser Ser Glu Val Asp Asn Trp Arg Ile Ile Pro Arg Asn Asn
                80          85          90

cca tcc agt gac tac cct agt gat ttt gag gtg att cag ata aaa gaa 820
Pro Ser Ser Asp Tyr Pro Ser Asp Phe Glu Val Ile Gln Ile Lys Glu
                95          100          105

aaa cag aaa gcg ggg ctg cta aca ctt gaa gat cat cca aac atc aaa 868
Lys Gln Lys Ala Gly Leu Leu Thr Leu Glu Asp His Pro Asn Ile Lys
                110          115          120

cgg gtc acg ccc caa cga aaa gtc ttt cgt tcc ctc aag tat gct gaa 916
Arg Val Thr Pro Gln Arg Lys Val Phe Arg Ser Leu Lys Tyr Ala Glu
                125          130          135          140

tct gac ccc aca gta ccc tgc aat gaa acc cgg tgg agc cag aag tgg 964
Ser Asp Pro Thr Val Pro Cys Asn Glu Thr Arg Trp Ser Gln Lys Trp
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caa tca tca cgt ccc ctg cga aga gcc agc ctc tcc ctg ggc tct ggc 1012
Gln Ser Ser Arg Pro Leu Arg Arg Ala Ser Leu Ser Leu Gly Ser Gly
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ttc tgg cat gct acg gga agg cat tcg agc aga cgg ctg ctg aga gcc 1060
Phe Trp His Ala Thr Gly Arg His Ser Ser Arg Arg Leu Leu Arg Ala
                175          180          185

atc ccg cgc cag gtt gcc cag aca ctg cag gca gat gtg ctc tgg cag 1108
Ile Pro Arg Gln Val Ala Gln Thr Leu Gln Ala Asp Val Leu Trp Gln
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## 10992\_29 ST25.txt

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ctg agc gag aag cat ccc cac ttc aaa aat gtg aag gag aga acc aac Leu Ser Glu Lys His Pro His Phe Lys Asn Val Lys Glu Arg Thr Asn 225 230 235	1204
tgg acc aac gag cga acg ctg gac gat ggg ttg ggc cat ggc aca ttc Trp Thr Asn Glu Arg Thr Leu Asp Asp Gly Leu Gly His Gly Thr Phe 240 245 250	1252
gtg gca ggt gtg ata gcc agc atg agg gag tgc caa gga ttt gct cca Val Ala Gly Val Ile Ala Ser Met Arg Glu Cys Gln Gly Phe Ala Pro 255 260 265	1300
gat gca gaa ctt cac att ttc agg gtc ttt acc aat aat cag gta tct Asp Ala Glu Leu His Ile Phe Arg Val Phe Thr Asn Asn Gln Val Ser 270 275 280	1348
tac aca tct tgg ttt ttg gac gcc ttc aac tat gcc att tta aag aag Tyr Thr Ser Trp Phe Leu Asp Ala Phe Asn Tyr Ala Ile Leu Lys Lys 285 290 295 300	1396
atc gac gtg tta aac ctc agc atc ggc ggc ccg gac ttc atg gat cat Ile Asp Val Leu Asn Leu Ser Ile Gly Gly Pro Asp Phe Met Asp His 305 310 315	1444
ccg ttt gtt gac aag gtg tgg gaa tta aca gct aac aat gta atc atg Pro Phe Val Asp Lys Val Trp Glu Leu Thr Ala Asn Asn Val Ile Met 320 325 330	1492
gtt tct gct att ggc aat gac gga cct ctt tat ggc act ctg aat aac Val Ser Ala Ile Gly Asn Asp Gly Pro Leu Tyr Gly Thr Leu Asn Asn 335 340 345	1540
cct gct gat caa atg gat gtg att gga gta ggc ggc att gac ttt gaa Pro Ala Asp Gln Met Asp Val Ile Gly Val Gly Gly Ile Asp Phe Glu 350 355 360	1588
gat aac atc gcc cgc ttt tct tca agg gga atg act acc tgg gag cta Asp Asn Ile Ala Arg Phe Ser Ser Arg Gly Met Thr Thr Trp Glu Leu 365 370 375 380	1636
cca gga ggc tac ggt cgc atg aaa cct gac att gtc acc tat ggt gct Pro Gly Gly Tyr Gly Arg Met Lys Pro Asp Ile Val Thr Tyr Gly Ala 385 390 395	1684
ggc gtg cgg ggt tct ggc gtg aaa ggg ggg tgc cgg gcc ctc tca ggg Gly Val Arg Gly Ser Gly Val Lys Gly Gly Cys Arg Ala Leu Ser Gly 400 405 410	1732
acc agt gtt gct tct cca gtg gtt gca ggt gct gtc acc ttg tta gtg Thr Ser Val Ala Ser Pro Val Val Ala Gly Ala Val Thr Leu Leu Val 415 420 425	1780
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gcc ctg atc gcg tca gcc cgg agg ctc ccc ggg gtc aac atg ttt gag 445 450 455 460 465 470 475 480 485 490 495	1876

## 10992\_29 ST25.txt

Ala 445	Leu	Ile	Ala	Ser	Ala 450	Arg	Arg	Leu	Pro	Gly 455	Val	Asn	Met	Phe	Glu 460	
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Gln	Gly	His	Gly	Lys 465	Leu	Asp	Leu	Leu	Arg 470	Ala	Tyr	Gln	Ile	Leu 475	Asn	
agc	tac	aag	cca	cag	gca	agt	ttg	agc	ccc	agc	tac	ata	gat	ctg	act	1972
Ser	Tyr	Lys	Pro 480	Gln	Ala	Ser	Leu	Ser 485	Pro	Ser	Tyr	Ile	Asp 490	Leu	Thr	
gag	tgt	ccc	tac	atg	tgg	ccc	tac	tgc	tcc	cag	ccc	atc	tac	tat	gga	2020
Glu	Cys	Pro 495	Tyr	Met	Trp	Pro	Tyr 500	Cys	Ser	Gln	Pro	Ile 505	Tyr	Tyr	Gly	
gga	atg	ccg	aca	gtt	gtt	aat	gtc	acc	atc	ctc	aac	ggc	atg	gga	gtc	2068
Gly	Met 510	Pro	Thr	Val	Val	Asn 515	Val	Thr	Ile	Leu	Asn 520	Gly	Met	Gly	Val	
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Thr	Gly	Arg	Ile	Val	Asp 530	Lys	Pro	Asp	Trp	Gln 535	Pro	Tyr	Leu	Pro	Gln 540	
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Asn	Gly	Asp	Asn	Ile 545	Glu	Val	Ala	Phe	Ser 550	Tyr	Ser	Ser	Val	Leu 555	Trp	
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Pro	Trp	Ser	Gly 560	Tyr	Leu	Ala	Ile	Ser 565	Ile	Ser	Val	Thr	Lys 570	Lys	Ala	
gct	tcc	tgg	gaa	ggc	att	gct	cag	ggc	cat	gtc	atg	atc	act	gtg	gct	2260
Ala	Ser	Trp 575	Glu	Gly	Ile	Ala	Gln 580	Gly	His	Val	Met	Ile 585	Thr	Val	Ala	
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Ser	Pro 590	Ala	Glu	Thr	Glu	Ser 595	Lys	Asn	Gly	Ala	Glu 600	Gln	Thr	Ser	Thr	
gta	aag	ctc	ccc	att	aag	gtg	aag	ata	att	cct	act	ccc	ccg	cga	agc	2356
Val	Lys	Leu	Pro	Ile	Lys 610	Val	Lys	Ile	Ile	Pro 615	Thr	Pro	Pro	Arg	Ser 620	
aag	aga	gtt	ctc	tgg	gat	cag	tac	cac	aac	ctc	cgc	tat	cca	cct	ggc	2404
Lys	Arg	Val	Leu	Trp 625	Asp	Gln	Tyr	His	Asn 630	Leu	Arg	Tyr	Pro	Pro 635	Gly	
tat	ttc	ccc	agg	gat	aat	tta	agg	atg	aag	aat	gac	cct	tta	gac	tgg	2452
Tyr	Phe	Pro	Arg 640	Asp	Asn	Leu	Arg	Met 645	Lys	Asn	Asp	Pro	Leu 650	Asp	Trp	
aat	ggt	gat	cac	atc	cac	acc	aat	ttc	agg	gat	atg	tac	cag	cat	ctg	2500
Asn	Gly	Asp 655	His	Ile	His	Thr	Asn 660	Phe	Arg	Asp	Met	Tyr 665	Gln	His	Leu	
aga	agc	atg	ggc	tac	ttt	gta	gag	gtc	ctc	ggg	gcc	ccc	ttc	acg	tgt	2548
Arg	Ser	Met	Gly	Tyr	Phe	Val 675	Glu	Val	Leu	Gly	Ala 680	Pro	Phe	Thr	Cys	
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Phe 685	Asp	Ala	Ser	Gln	Tyr 690	Gly	Thr	Leu	Leu	Met 695	Val	Asp	Ser	Glu	Glu 700	

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Glu Tyr Phe Pro Glu Ile Ala Lys Leu Arg Arg Asp Val Asp Asn	
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ggc ctc tcg ctc gtc atc ttc agt gac tgg tac aac act tct gtt atg	2692
Gly Leu Ser Leu Val Ile Phe Ser Asp Trp Tyr Asn Thr Ser Val Met	
720 725 730	
aga aaa gtg aag ttt tat gat gaa aac aca agg cag tgg tgg atg ccg	2740
Arg Lys Val Lys Phe Tyr Asp Glu Asn Thr Arg Gln Trp Trp Met Pro	
735 740 745	
gat acc gga gga gct aac atc cca gct ctg aat gag ctg ctg tct gtg	2788
Asp Thr Gly Gly Ala Asn Ile Pro Ala Leu Asn Glu Leu Leu Ser Val	
750 755 760	
tgg aac atg ggg ttc agc gat ggc ctg tat gaa ggg gag ttc acc ctg	2836
Trp Asn Met Gly Phe Ser Asp Gly Leu Tyr Glu Gly Glu Phe Thr Leu	
765 770 775 780	
gcc aac cat gac atg tat tat gcg tca ggg tgc agc atc gcg aag ttt	2884
Ala Asn His Asp Met Tyr Tyr Ala Ser Gly Cys Ser Ile Ala Lys Phe	
785 790 795	
cca gaa gat ggc gtc gtg ata aca cag act ttc aag gac caa gga ttg	2932
Pro Glu Asp Gly Val Val Ile Thr Gln Thr Phe Lys Asp Gln Gly Leu	
800 805 810	
gag gtt tta aag cag gaa aca gca gtt gtt gaa aac gtc ccc att ttg	2980
Glu Val Leu Lys Gln Glu Thr Ala Val Val Glu Asn Val Pro Ile Leu	
815 820 825	
gga ctt tat cag att cca gct gag ggt gga ggc cgg att gta ctg tat	3028
Gly Leu Tyr Gln Ile Pro Ala Glu Gly Gly Gly Arg Ile Val Leu Tyr	
830 835 840	
ggg gac tcc aat tgc ttg gat gac agt cac cga cag aag gac tgc ttt	3076
Gly Asp Ser Asn Cys Leu Asp Asp Ser His Arg Gln Lys Asp Cys Phe	
845 850 855 860	
tgg ctt ctg gat gcc ctc ctc cag tac aca tcg tat ggg gtg aca ccg	3124
Trp Leu Leu Asp Ala Leu Leu Gln Tyr Thr Ser Tyr Gly Val Thr Pro	
865 870 875	
cct agc ctc agt cac tct ggg aac cgc cag cgc cct ccc agt gga gca	3172
Pro Ser Leu Ser His Ser Gly Asn Arg Gln Arg Pro Pro Ser Gly Ala	
880 885 890	
ggc tca gtc act cca gag agg atg gaa gga aac cat ctt cat cgg tac	3220
Gly Ser Val Thr Pro Glu Arg Met Glu Gly Asn His Leu His Arg Tyr	
895 900 905	
tcc aag gtt ctg gag gcc cat ttg gga gac cca aaa cct cgg cct cta	3268
Ser Lys Val Leu Glu Ala His Leu Gly Asp Pro Lys Pro Arg Pro Leu	
910 915 920	
cca gcc tgt cca cgc ttg tct tgg gcc aag cca cag cct tta aac gag	3316
Pro Ala Cys Pro Arg Leu Ser Trp Ala Lys Pro Gln Pro Leu Asn Glu	
925 930 935 940	
acg gcg ccc agt aac ctt tgg aaa cat cag aag cta ctc tcc att gac	3364

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Thr	Ala	Pro	Ser	Asn	Leu	Trp	Lys	His	Gln	Lys	Leu	Leu	Ser	Ile	Asp			
				945					950					955				
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agg	ccc	ttg	tcc	cct	gga	gag	agc	ggc	gcc	tgg	gac	att	cct	gga	ggg	3460		
Arg	Pro	Leu	Ser	Pro	Gly	Glu	Ser	Gly	Ala	Trp	Asp	Ile	Pro	Gly	Gly			
			975				980					985						
atc	atg	cct	ggc	cgc	tac	aac	cag	gag	gtg	ggc	cag	acc	att	cct	gtc	3508		
Ile	Met	Pro	Gly	Arg	Tyr	Asn	Gln	Glu	Val	Gly	Gln	Thr	Ile	Pro	Val			
	990					995					1000							
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Phe	Ala	Phe	Leu	Gly	Ala	Met	Val	Val	Leu	Ala	Phe	Phe	Val	Val				
1005					1010					1015								
caa	atc	aac	aag	gcc	aag	agc	agg	ccg	aag	cgg	agg	aag	ccc	agg		3598		
Gln	Ile	Asn	Lys	Ala	Lys	Ser	Arg	Pro	Lys	Arg	Arg	Lys	Pro	Arg				
1020					1025					1030								
gtg	aag	cgc	ccg	cag	ctc	atg	cag	cag	gtt	cac	ccg	cca	aag	acc		3643		
Val	Lys	Arg	Pro	Gln	Leu	Met	Gln	Gln	Val	His	Pro	Pro	Lys	Thr				
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cct	tcg	gtg	tgacc	ggcag	cctgg	ctgac	cgtgagggcc	agagagagcc								3692		
Pro	Ser	Val																
1050																		
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cagag	gctcc	tgg	tac	atcg	aga	agatt	cc	tgtg	gatccc	g	tcagg	aggg	acttag	tggc		3872		
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cag	tttttt	act	att	ccat	cat	gagga	aac	aac	atag	att	ccat	gat	ctt	ttta	atgaca		4172	
gtac	agact	g	agatt	tga	ag	gaa	acat	gca	caa	at	ctg	ta	aa	acat	agac	cttc	gcttta	4232
tttt	tga	ag	tat	cac	ctg	c	accat	gttt	t	gta	attt	gga	gg	tctt	gatt	tcacc	attgt	4292
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Gly Lys Lys His Leu Gly Asp Arg Leu Glu Lys Lys Ser Phe Glu Lys  
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Ala Pro Cys Pro Gly Cys Ser His Leu Thr Leu Lys Val Glu Phe Ser  
35 40 45

Ser Thr Val Val Glu Tyr Glu Tyr Ile Val Ala Phe Asn Gly Tyr Phe  
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Thr Ala Lys Ala Arg Asn Ser Phe Ile Ser Ser Ala Leu Lys Ser Ser  
65 70 75 80

Glu Val Asp Asn Trp Arg Ile Ile Pro Arg Asn Asn Pro Ser Ser Asp  
85 90 95

Tyr Pro Ser Asp Phe Glu Val Ile Gln Ile Lys Glu Lys Gln Lys Ala  
100 105 110

Gly Leu Leu Thr Leu Glu Asp His Pro Asn Ile Lys Arg Val Thr Pro  
115 120 125

Gln Arg Lys Val Phe Arg Ser Leu Lys Tyr Ala Glu Ser Asp Pro Thr  
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Val Pro Cys Asn Glu Thr Arg Trp Ser Gln Lys Trp Gln Ser Ser Arg  
145 150 155 160

Pro Leu Arg Arg Ala Ser Leu Ser Leu Gly Ser Gly Phe Trp His Ala  
165 170 175

Thr Gly Arg His Ser Ser Arg Arg Leu Leu Arg Ala Ile Pro Arg Gln  
180 185 190

Val Ala Gln Thr Leu Gln Ala Asp Val Leu Trp Gln Met Gly Tyr Thr  
195 200 205

Gly Ala Asn Val Arg Val Ala Val Phe Asp Thr Gly Leu Ser Glu Lys  
210 215 220

His Pro His Phe Lys Asn Val Lys Glu Arg Thr Asn Trp Thr Asn Glu  
225 230 235 240

Arg Thr Leu Asp Asp Gly Leu Gly His Gly Thr Phe Val Ala Gly Val  
245 250 255

Ile Ala Ser Met Arg Glu Cys Gln Gly Phe Ala Pro Asp Ala Glu Leu

260

270

His Ile Phe Arg Val Phe Thr Asn Asn Gln Val Ser Tyr Thr Ser Trp  
275 280 285

Phe Leu Asp Ala Phe Asn Tyr Ala Ile Leu Lys Lys Ile Asp Val Leu  
290 295 300

Asn Leu Ser Ile Gly Gly Pro Asp Phe Met Asp His Pro Phe Val Asp  
305 310 315 320

Lys Val Trp Glu Leu Thr Ala Asn Asn Val Ile Met Val Ser Ala Ile  
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Gly Asn Asp Gly Pro Leu Tyr Gly Thr Leu Asn Asn Pro Ala Asp Gln  
340 345 350

Met Asp Val Ile Gly Val Gly Gly Ile Asp Phe Glu Asp Asn Ile Ala  
355 360 365

Arg Phe Ser Ser Arg Gly Met Thr Thr Trp Glu Leu Pro Gly Gly Tyr  
370 375 380

Gly Arg Met Lys Pro Asp Ile Val Thr Tyr Gly Ala Gly Val Arg Gly  
385 390 395 400

Ser Gly Val Lys Gly Gly Cys Arg Ala Leu Ser Gly Thr Ser Val Ala  
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Ser Pro Val Val Ala Gly Ala Val Thr Leu Leu Val Ser Thr Val Gln  
420 425 430

Lys Arg Glu Leu Val Asn Pro Ala Ser Met Lys Gln Ala Leu Ile Ala  
435 440 445

Ser Ala Arg Arg Leu Pro Gly Val Asn Met Phe Glu Gln Gly His Gly  
450 455 460

Lys Leu Asp Leu Leu Arg Ala Tyr Gln Ile Leu Asn Ser Tyr Lys Pro  
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Gln Ala Ser Leu Ser Pro Ser Tyr Ile Asp Leu Thr Glu Cys Pro Tyr  
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Met Trp Pro Tyr Cys Ser Gln Pro Ile Tyr Tyr Gly Gly Met Pro Thr  
500 505 510

Val Val Asn Val Thr Ile Leu Asn Gly Met Gly Val Thr Gly Arg Ile  
 515 520 525

Val Asp Lys Pro Asp Trp Gln Pro Tyr Leu Pro Gln Asn Gly Asp Asn  
 530 535 540

Ile Glu Val Ala Phe Ser Tyr Ser Ser Val Leu Trp Pro Trp Ser Gly  
 545 550 555 560

Tyr Leu Ala Ile Ser Ile Ser Val Thr Lys Lys Ala Ala Ser Trp Gly  
 565 570 575

Gly Ile Ala Gln Gly His Val Met Ile Thr Val Ala Ser Pro Ala Glu  
 580 585 590

Thr Glu Ser Lys Asn Gly Ala Glu Gln Thr Ser Thr Val Lys Leu Pro  
 595 600 605

Ile Lys Val Lys Ile Ile Pro Thr Pro Pro Arg Ser Lys Arg Val Leu  
 610 615 620

Trp Asp Gln Tyr His Asn Leu Arg Tyr Pro Pro Gly Tyr Phe Pro Arg  
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Asp Asn Leu Arg Met Lys Asn Asp Pro Leu Asp Trp Asn Gly Asp His  
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Ile His Thr Asn Phe Arg Asp Met Tyr Gln His Leu Arg Ser Met Gly  
 660 665 670

Tyr Phe Val Glu Val Leu Gly Ala Pro Phe Thr Cys Phe Asp Ala Ser  
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Gln Tyr Gly Thr Leu Leu Met Val Asp Ser Glu Glu Glu Tyr Phe Pro  
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Glu Glu Ile Ala Lys Leu Arg Arg Asp Val Asp Asn Gly Leu Ser Leu  
 705 710 715 720

Val Ile Phe Ser Asp Trp Tyr Asn Thr Ser Val Met Arg Lys Val Lys  
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Phe Tyr Asp Glu Asn Thr Arg Gln Trp Trp Met Pro Asp Thr Gly Gly  
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Ala Asn Ile Pro Ala Leu Asn Glu Leu Leu Ser Val Trp Asn Met Gly  
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Phe Ser Asp Gly Leu Tyr Glu Gly Glu Phe Thr Leu Ala Asn His Asp  
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 Met Tyr Tyr Ala Ser Gly Cys Ser Ile Ala Lys Phe Pro Glu Asp Gly  
 785 790 795 800  
 Val Val Ile Thr Gln Thr Phe Lys Asp Gln Gly Leu Glu Val Leu Lys  
 805 810 815  
 Gln Glu Thr Ala Val Val Glu Asn Val Pro Ile Leu Gly Leu Tyr Gln  
 820 825 830  
 Ile Pro Ala Glu Gly Gly Gly Arg Ile Val Leu Tyr Gly Asp Ser Asn  
 835 840 845  
 Cys Leu Asp Asp Ser His Arg Gln Lys Asp Cys Phe Trp Leu Leu Asp  
 850 855 860  
 Ala Leu Leu Gln Tyr Thr Ser Tyr Gly Val Thr Pro Pro Ser Leu Ser  
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 His Ser Gly Asn Arg Gln Arg Pro Pro Ser Gly Ala Gly Ser Val Thr  
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 Pro Glu Arg Met Glu Gly Asn His Leu His Arg Tyr Ser Lys Val Leu  
 900 905 910  
 Glu Ala His Leu Gly Asp Pro Lys Pro Arg Pro Leu Pro Ala Cys Pro  
 915 920 925  
 Arg Leu Ser Trp Ala Lys Pro Gln Pro Leu Asn Glu Thr Ala Pro Ser  
 930 935 940  
 Asn Leu Trp Lys His Gln Lys Leu Leu Ser Ile Asp Leu Asp Lys Val  
 945 950 955 960  
 Val Leu Pro Asn Phe Arg Ser Asn Arg Pro Gln Val Arg Pro Leu Ser  
 965 970 975  
 Pro Gly Glu Ser Gly Ala Trp Asp Ile Pro Gly Gly Ile Met Pro Gly  
 980 985 990  
 Arg Tyr Asn Gln Glu Val Gly Gln Thr Ile Pro Val Phe Ala Phe Leu  
 995 1000 1005  
 Gly Ala Met Val Val Leu Ala Phe Phe Val Val Gln Ile Asn Lys

1010

1015

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 <222> (4)..(7)  
 <223> Xaa represents any amino acid

<220>  
 <221> VARIANT  
 <222> (8)..(8)  
 <223> Xaa represents an acidic amino acid

<400> 9

Arg Xaa Xaa Xaa Xaa Xaa Xaa Xaa  
 1 5

<210> 10  
 <211> 8  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Peptide substrate

<220>  
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 <223> Xaa represents any amino acid

<220>  
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 <222> (3)..(3)  
 <223> Xaa represents an alkyl or aromatic hydrophobic amino acid

<220>  
 <221> VARIANT  
 <222> (4)..(4)  
 <223> Xaa represents Lys, Leu, Phe or Thr

<220>  
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 <223> Xaa represents any amino acid

<220>  
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 <223> Xaa represents an acidic amino acid

<400> 10

Arg Xaa Xaa Xaa Xaa Xaa Xaa Xaa  
 1 5

<210> 11  
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<220>  
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<220>

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<220>  
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<400> 11

Arg Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa  
 1 5

<210> 12  
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<220>  
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<220>  
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 <223> Xaa represents any amino acid

<220>  
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 <222> (9)..(9)  
 <223> Xaa represents an acidic amino acid

<400> 12

Arg Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa  
 1 5

<210> 13  
 <211> 11  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Peptide substrate



&lt;400&gt; 13

Val Phe Arg Ser Leu Lys Tyr Ala Glu Ser Asp  
 1 5 10

&lt;210&gt; 14

&lt;211&gt; 13

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Peptide substrate

&lt;220&gt;

&lt;221&gt; Modified\_res

&lt;222&gt; (1)..(1)

&lt;223&gt; Xaa represents orthoaminobenzoic acid

&lt;220&gt;

&lt;221&gt; Modified\_res

&lt;222&gt; (13)..(13)

&lt;223&gt; Xaa represents 3-nitrotyrosine

&lt;400&gt; 14

Xaa Val Phe Arg Ser Leu Lys Tyr Ala Glu Ser Asp Xaa  
 1 5 10

&lt;210&gt; 15

&lt;211&gt; 23

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; oligonucleotide

&lt;220&gt;

&lt;221&gt; variation

&lt;222&gt; (3)..(3)

&lt;223&gt; i

&lt;220&gt;

&lt;221&gt; variation

&lt;222&gt; (9)..(9)

&lt;223&gt; i

&lt;220&gt;

&lt;221&gt; variation

&lt;222&gt; (12)..(12)

&lt;223&gt; i

&lt;220&gt;

&lt;221&gt; variation

&lt;222&gt; (18)..(18)

&lt;223&gt; i

&lt;220&gt;

&lt;221&gt; variation

&lt;222&gt; (21)..(21)

<223> i

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23

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<223> i

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<222> (18)..(18)  
<223> i

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<222> (21)..(21)  
<223> i

<220>  
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<222> (24)..(24)  
<223> i

<220>  
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<222> (29)..(29)  
<223> i

<400> 16  
ccngynacnw snggnswngc nacnswgtnc c

31

<210> 17  
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 <223> Xaa represent histidine or phenylalanine

<220>  
 <221> VARIANT  
 <222> (6)..(6)  
 <223> Xaa represents valine or cysteine

<400> 17

Gly His Gly Thr Xaa Xaa Ala Gly  
 1 5

<210> 18  
 <211> 11  
 <212> PRT  
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<220>  
 <223> Peptide substrate

<220>  
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 <222> (4)..(4)  
 <223> Xaa represents valine or methionine

<220>  
 <221> VARIANT  
 <222> (6)..(6)  
 <223> Xaa represents threonine or serine

<220>  
 <221> VARIANT  
 <222> (8)..(8)  
 <223> Xaa represents histidine or valine

<220>  
 <221> VARIANT  
 <222> (10)..(10)  
 <223> Xaa represents alanine or threonine

<400> 18

Gly Thr Ser Xaa Ala Xaa Pro Xaa Val Xaa Gly  
 1 5 10

<210> 19

<211> 28  
 <212> DNA  
 <213> Artificial Sequence

<220>  
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 ggatccgaag aaacatctgg gcgacaga

28

<210> 20  
 <211> 24  
 <212> DNA  
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<220>  
 <223> Primer

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 ctcgagggct ctcagccgtg tgct

24

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 <212> DNA  
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<220>  
 <223> Primer

<400> 21  
 gaggaagaga cagggataaa c

21

<210> 22  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Primer

<400> 22  
 gggatatgct tagcattgac

20

<210> 23  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Primer

<400> 23  
 agccctatta cctgaacctg

20

<210> 24  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence

<220>  
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 <400> 24  
 gaatctgaaa gaactccccc 20

<210> 25  
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<220>  
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 ttccgagatt ccacccctacg 20

<210> 26  
 <211> 20  
 <212> DNA  
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<220>  
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<210> 27  
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 <212> DNA  
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<220>  
 <223> Primer  
 <400> 27  
 tctcctccaa cctcaaccac 20

<210> 28  
 <211> 22  
 <212> DNA  
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<220>  
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 ccagcctgtc atcctcaata tc 22

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<220>

<223> Primer

<400> 29

ggagccatgg attgcacttt c

21

<210> 30

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 30

aggagctcaa tgtggcagga

20

<210> 31

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 31

gtgaccatga agcttgtaa catctgg

27

<210> 32

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 32

acactgggtcc ctgagagggc ccggca

26

<210> 33

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 33

attgacctgg acaaggtggt g

21

<210> 34

<211> 57

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

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ggatcctcta gatcagtggg ggtggtggtg gtggtgctcc tggttgtagc ggccagg

57

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<220>  
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24

<210> 36  
 <211> 28  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Primer

<400> 36  
 ctcgagtgtc tgggcaacct ggcgcggg

28

<210> 37  
 <211> 14  
 <212> PRT  
 <213> Homo sapiens

<400> 37

Lys Ala Gly Ser Arg Gly Leu Thr Ser Leu Ala Asp Thr Phe  
 1 5 10

<210> 38  
 <211> 27  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Peptide Substrate

<400> 38

Gly Gly Ala His Asp Ser Asp Gln His Pro His Ser Gly Ser Gly Arg  
 1 5 10 15

Ser Val Leu Ser Phe Glu Ser Gly Ser Gly Gly  
 20 25

<210> 39  
 <211> 18  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Peptide Substrate

<400> 39

Trp His Ala Thr Gly Arg His Ser Ser Arg Arg Leu Leu Arg Ala Ile  
1 5 10 15

Pro Arg

<210> 40

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> Peptide Substrate

<400> 40

Trp His Ala Thr Gly Arg His Ser Ser Arg Arg Leu Leu Arg Ala Leu  
1 5 10 15

Glu

<210> 41

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Peptide Substrate

<400> 41

Ser Arg Arg Leu Leu Arg Ala Leu Glu  
1 5

<210> 42

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> Peptide Substrate

<400> 42

Trp Gln Ser Ser Arg Pro Leu Arg Arg Ala Ser Leu Ser Leu Gly Ser  
1 5 10 15

Gly



<210> 43  
 <211> 15  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Peptide Substrate

<400> 43

Arg Ala Ile Pro Arg Gln Val Ala Gln Thr Leu Gln Ala Asp Val  
 1 5 10 15

<210> 44  
 <211> 9  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Peptide Substrate

<400> 44

Pro Gln Arg Lys Val Phe Arg Ser Leu  
 1 5

<210> 45  
 <211> 15  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Peptide Substrate

<400> 45

Pro Gln Arg Lys Val Phe Arg Ser Leu Lys Tyr Ala Glu Ser Asp  
 1 5 10 15

<210> 46  
 <211> 14  
 <212> PRT  
 <213> Artificial Sequence

<220>  
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<220>  
 <221> MOD\_RES  
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 <223> Xaa represents orthoaminobenzoic acid

<220>  
 <221> MOD\_RES  
 <222> (13)..(13)  
 <223> Xaa represents 3-nitrotyrosine

<400> 46

10992\_29 ST25.txt

Xaa Val Phe Arg Ser Leu Lys Tyr Ala Glu Ser Asp Xaa Ala  
1 5 10

<210> 47  
<211> 12  
<212> PRT  
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<223> Xaa represents orthoaminobenzoic acid

<220>  
<221> MOD\_RES  
<222> (11)..(11)  
<223> Xaa represents 3-nitrotyrosine

<400> 47

Xaa Arg Ser Leu Lys Tyr Ala Glu Ser Asp Xaa Ala  
1 5 10

<210> 48  
<211> 16  
<212> PRT  
<213> Homo sapiens

<400> 48

Lys Ala Gly Ser Arg Gly Leu Thr Ser Leu Ala Asp Thr Phe Glu His  
1 5 10 15

<210> 49  
<211> 16  
<212> PRT  
<213> Rattus sp.

<400> 49

Lys Ala Gly Ser Arg Gly Leu Thr Thr Thr Ser Leu Ala Asp Thr Phe  
1 5 10 15

<210> 50  
<211> 16  
<212> PRT  
<213> Homo sapiens

<400> 50

Arg His Ser Ser Arg Arg Leu Leu Arg Ala Ile Pro Arg Gln Val Ala  
1 5 10 15

<210> 51  
 <211> 16  
 <212> PRT  
 <213> Homo sapiens

<400> 51

Arg Lys Val Phe Arg Ser Leu Lys Tyr Ala Glu Ser Asp Pro Thr Val  
 1 5 10 15

<210> 52  
 <211> 16  
 <212> PRT  
 <213> Homo sapiens

<400> 52

Thr Pro Gln Arg Lys Val Phe Arg Ser Leu Lys Tyr Ala Glu Ser Asp  
 1 5 10 15

<210> 53  
 <211> 16  
 <212> PRT  
 <213> Homo sapiens

<400> 53

Val Thr Pro Gln Arg Lys Val Phe Arg Ser Leu Lys Lys Tyr Ala Glu  
 1 5 10 15

<210> 54  
 <211> 16  
 <212> PRT  
 <213> Homo sapiens

<400> 54

Ser Gly Ser Gly Arg Ser Val Leu Ser Phe Glu Ser Gly Ser Gly Gly  
 1 5 10 15

<210> 55  
 <211> 16  
 <212> PRT  
 <213> Homo sapiens

<400> 55

His Ser Pro Gly Arg Asn Val Leu Gly Thr Glu Ser Arg Asp Gly Pro  
 1 5 10 15

<210> 56  
 <211> 16  
 <212> PRT  
 <213> Rattus sp.

<400> 56

Ala Ser Val Gly Arg Leu Ala Leu Ser Gln Glu Glu Pro Ala Pro Leu  
 Page 43

1 5 10 15

<210> 57  
 <211> 16  
 <212> PRT  
 <213> Homo sapiens

<400> 57

Arg Ile Ser Asp Arg Asp Tyr Met Gly Trp Met Asp Phe Gly Arg Arg  
 1 5 10 15

<210> 58  
 <211> 16  
 <212> PRT  
 <213> Rattus sp.

<400> 58

Asp Pro Arg Leu Arg Gln Phe Leu Gln Lys Ser Leu Ala Ala Ala Thr  
 1 5 10 15

<210> 59  
 <211> 16  
 <212> PRT  
 <213> Bovis sp.

<400> 59

Leu Leu Lys Glu Leu Gln Asp Leu Ala Leu Gln Gly Ala Lys Glu Arg  
 1 5 10 15

<210> 60  
 <211> 16  
 <212> PRT  
 <213> Bovis sp.

<400> 60

Met Ala Arg Ala Pro Gln Val Leu Phe Arg Gly Gly Lys Ser Gly Glu  
 1 5 10 15

<210> 64  
 <211> 16  
 <212> PRT  
 <213> Bovis sp.

<400> 61

Glu Leu Glu Asn Leu Ala Ala Met Asp Leu Glu Leu Gln Lys Ile Ala  
 1 5 10 15

<210> 62  
 <211> 16  
 <212> PRT  
 <213> Bovis sp.

&lt;400&gt; 62

Ala	Ala	Met	Asp	Leu	Glu	Leu	Gln	Lys	Ile	Ala	Glu	Lys	Phe	Ser	Gly
1				5					10					15	

&lt;210&gt; 63

&lt;211&gt; 16

&lt;212&gt; PRT

&lt;213&gt; Rattus sp.

&lt;400&gt; 63

Lys	Ser	Ser	Phe	Thr	Asn	Val	Thr	Ser	Pro	Val	Val	Leu	Thr	Asn	Tyr
1				5					10					15	

&lt;210&gt; 64

&lt;211&gt; 16

&lt;212&gt; PRT

&lt;213&gt; Rattus sp.

&lt;400&gt; 64

Lys	Ser	Gln	Thr	Pro	Leu	Val	Thr	Leu	Phe	Lys	Asn	Ala	Ile	Ile	Lys
1				5					10					15	

&lt;210&gt; 65

&lt;211&gt; 16

&lt;212&gt; PRT

&lt;213&gt; Rattus sp.

&lt;400&gt; 65

Ser	Gln	Thr	Pro	Leu	Val	Thr	Leu	Phe	Lys	Asn	Ala	Ile	Ile	Lys	Asn
1				5					10					15	

&lt;210&gt; 66

&lt;211&gt; 16

&lt;212&gt; PRT

&lt;213&gt; Rattus sp.

&lt;400&gt; 66

Gly	Pro	Ala	Arg	Glu	Leu	Leu	Leu	Arg	Leu	Val	Gln	Leu	Ala	Gly	Thr
1				5					10					15	

&lt;210&gt; 67

&lt;211&gt; 16

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 67

Leu	Leu	Arg	Lys	Lys	Arg	Thr	Thr	Ser	Ala	Glu	Lys	Asn	Thr	Cys	Gln
1				5					10					15	

&lt;210&gt; 68

<211> 16  
 <212> PRT  
 <213> Homo sapiens

<400> 68

Glu Glu Ile Ser Glu Val Lys Met Asp Ala Glu Phe Arg His Asp Ser  
 1 5 10 15

<210> 69  
 <211> 16  
 <212> PRT  
 <213> Homo sapiens

<400> 69

Glu Glu Ile Ser Glu Val Asn Leu Asp Ala Glu Phe Arg His Asp Ser  
 1 5 10 15

<210> 70  
 <211> 16  
 <212> PRT  
 <213> Homo sapiens

<400> 70

Ile Ser Glu Val Lys Met Asp Ala Glu Phe Arg His Asp Ser Gly Tyr  
 1 5 10 15

<210> 71  
 <211> 16  
 <212> PRT  
 <213> Homo sapiens

<400> 71

Glu Phe Arg His Asp Ser Gly Tyr Glu Val His His Gln Lys Leu Val  
 1 5 10 15

<210> 72  
 <211> 10  
 <212> PRT  
 <213> Artificial sequence

<220>  
 <223> Peptide substrate

<400> 72

Ser Ser Arg Arg Leu Leu Arg Ala Ile Glu  
 1 5 10

<210> 73  
 <211> 12  
 <212> PRT  
 <213> Artificial sequence

<220>

<223> Peptide Substrate

<400> 73

Ser Gly Ser Gly Arg Ser Val Leu Ser Phe Glu Ser  
1 5 10

<210> 74

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> Peptide Substrate

<220>

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<222> (1)..(1)

<223> Xaa represents orthoaminobenzoic acid

<220>

<221> MOD\_RES

<222> (13)..(13)

<223> Xaa represents 3-nitrotyrosine

<400> 74

Xaa Arg His Ser Ser Arg Arg Leu Leu Arg Ala Ile Xaa Ala  
1 5 10

<210> 75

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> Peptide Substrate

<220>

<221> MOD\_RES

<222> (1)..(1)

<223> Xaa represents orthoaminobenzoic acid

<220>

<221> MOD\_RES

<222> (11)..(11)

<223> Xaa represents 3-nitrotyrosine

<400> 75

Xaa Ser Arg Arg Leu Leu Arg Ala Leu Glu Xaa Ala  
1 5 10

<210> 76

<211> 15

<212> PRT

<213> Artificial Sequence

<220>  
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 <222> (1)..(1)  
 <223> Xaa represents orthoaminobenzoic acid

<220>  
 <221> MOD\_RES  
 <222> (14)..(14)  
 <223> Xaa represents 3-nitrotyrosine

<400> 76

Xaa Asn Gly Pro Lys Ala Gly Ser Arg Gly Leu Thr Ser Xaa Ala  
 1 5 10 15

<210> 77  
 <211> 13  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Consensus sequence for growth factors

<400> 77

Cys Leu Asp Asp Ser His Arg Gln Lys Asp Cys Phe Trp  
 1 5 10

<210> 78  
 <211> 9  
 <212> PRT  
 <213> Homo sapiens

<400> 78

Gly Cys Met Leu Ala Ala Pro Met Lys  
 1 5

<210> 79  
 <211> 18  
 <212> PRT  
 <213> Homo sapiens

<400> 79

Arg Gly Leu Thr Ser Leu Ala Asp Thr Phe Glu His Val Ile Glu Glu  
 1 5 10 15

Leu Leu

<210> 80  
 <211> 10



<212> PRT  
 <213> Homo sapiens

<400> 80

Lys Ala Gly Ser Arg Gly Leu Thr Ser Leu  
 1 5 10

<210> 81  
 <211> 10  
 <212> PRT  
 <213> Homo sapiens

<400> 81

Gln Cys Leu Cys Val Lys Thr Thr Ser Gln  
 1 5 10

<210> 82  
 <211> 10  
 <212> PRT  
 <213> Homo sapiens

<400> 82

Lys Gly Pro Trp Cys Phe Thr Thr Asp Pro  
 1 5 10

<210> 83  
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 <213> Homo sapiens

<400> 83

Lys Ser Gln Thr Pro Leu Val Thr Leu Phe  
 1 5 10

<210> 84  
 <211> 10  
 <212> PRT  
 <213> Homo sapiens

<400> 84

Leu Leu Arg Lys Lys Arg Thr Thr Ser Ala  
 1 5 10

<210> 85  
 <211> 10  
 <212> PRT  
 <213> Homo sapiens

<400> 85

Val Gly Gly Val Val Ile Ala Thr Val Ile  
 1 5 10

<210> 86  
 <211> 8  
 <212> PRT  
 <213> Mus sp.

<400> 86

Arg Gly Leu Thr Thr Thr Ser Leu  
 1 5

<210> 87  
 <211> 11  
 <212> PRT  
 <213> Sus sp.

<400> 78

Arg Gly Leu Thr Ser Ser Ser Ser Ser Ser Leu  
 1 5 10

<210> 88  
 <211> 10  
 <212> PRT  
 <213> Homo sapiens

<400> 88

Arg Asn Asn Pro Ser Ser Asp Tyr Pro Ser  
 1 5 10

<210> 89  
 <211> 8  
 <212> PRT  
 <213> Homo sapiens

<400> 89

Arg His Ser Ser Arg Arg Leu Leu  
 1 5

<210> 90  
 <211> 4  
 <212> PRT  
 <213> Homo sapiens

<400> 90

Arg Arg Leu Leu  
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<210> 91  
 <211> 13  
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 <213> Artificial sequence

<220>  
 <223> Fragment resulting from cloning

&lt;400&gt; 91

Pro Gly Arg Tyr Asn Gln Glu His His His His His His  
 1 5 10

&lt;210&gt; 92

&lt;211&gt; 12

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 92

Leu Val Val Leu Leu Cys Gly Lys Lys His Leu Gly  
 1 5 10

&lt;210&gt; 93

&lt;211&gt; 19

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 93

Lys Tyr Ala Glu Ser Asp Pro Thr Val Pro Cys Asn Glu Thr Arg Trp  
 1 5 10 15

Ser Gln Lys

&lt;210&gt; 94

&lt;211&gt; 8

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 94

Arg Lys Val Phe Arg Ser Leu Lys  
 1 5

&lt;210&gt; 95

&lt;211&gt; 7

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 95

Gly Lys Lys Arg Lys Val Phe  
 1 5

&lt;210&gt; 96

&lt;211&gt; 8

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 96

Gly Lys Lys Arg Lys Val Phe Arg  
1 5

<210> 97  
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Gly Lys Lys Arg Lys Val Phe Arg Ser Leu  
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Gly Lys Lys Arg Lys Val Phe Arg Ser Leu Lys  
1 5 10

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Arg Gly Leu Thr Ser Leu  
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Arg Ser Leu Lys  
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&lt;400&gt; 101

Xaa Val Phe Arg Ser Leu Lys  
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&lt;211&gt; 5

&lt;212&gt; PRT

&lt;213&gt; Artificial sequence

&lt;220&gt;

&lt;223&gt; Fluorescent candidate substrate

&lt;220&gt;

&lt;221&gt; VARIANT

&lt;222&gt; (1)..(1)

&lt;223&gt; Xaa represents Abz

&lt;400&gt; 102

Xaa Arg Ser Leu Lys  
 1 5

&lt;210&gt; 103

&lt;211&gt; 7

&lt;212&gt; PRT

&lt;213&gt; Artificial sequence

&lt;220&gt;

&lt;223&gt; Non fluorescent candidate substrate

&lt;220&gt;

&lt;221&gt; VARIANT

&lt;222&gt; (6)..(6)

&lt;223&gt; Xaa represents Y(NO2)

&lt;400&gt; 103

Tyr Ala Glu Ser Asp Xaa Ala  
 1 5

&lt;210&gt; 104

&lt;211&gt; 8

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 104

Arg Arg Leu Leu Arg Ala Ile Pro  
 1 5

&lt;210&gt; 105

&lt;211&gt; 8

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 105

Arg Ser Leu Lys Tyr Ala Glu Ser  
1 5

<210> 106  
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<400> 106

Arg Arg Leu Leu Arg Ala  
1 5

<210> 107  
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Xaa Arg Ser Leu Lys Tyr Ala Glu Ser Asp Xaa  
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<400> 108

Gln Arg Lys Val Phe Arg Ser Leu Lys Tyr Ala Glu  
1 5 10

58

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